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PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,202

DATE: 03/28/2002
TIME: 14:04:31

Error on pp. 1-4

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\03282002\J088202.raw

3 <110> APPLICANT: MOGAM BIOTECHNOLOGY RESEARCH INSTITUTE
5 <120> TITLE OF INVENTION: NOVEL DETOXIFIED MUTANTS OF Escherichia coli HEAT-LABILE
6 ENTEROTOXIN
8 <130> FILE REFERENCE: 2p-03-12
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/088,202
C--> 10 <141> CURRENT FILING DATE: 2002-03-15
10 <160> NUMBER OF SEQ ID NOS: 6
12 <170> SOFTWARE: KopatentIn 1.71

ERRORED SEQUENCES

40 <210> SEQ ID NO: 3
41 <211> LENGTH: 382
42 <212> TYPE: PRT
43 <213> ORGANISM: Escherichia coli
45 <220> FEATURE:
46 <221> NAME/KEY: SIGNAL
47 <222> LOCATION: (-18)..(-1)
49 <400> SEQUENCE: 3

50 Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
E--> 51 -18 -14 -9
E--> 52 -4
54 Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
E--> 55 2 7
57 Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
E--> 58 17 22 27
60 Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Tyr Ala Asn Gly Asp Arg
E--> 61 32 37 42
63 Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
E--> 64 47 52 57
66 Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Phe Asp Arg Gly Thr Glu Met
E--> 67 67 72
69 Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Gly Thr Gln Thr Gly Phe Val
E--> 70 82 87 92
72 Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Ser Leu Ser Leu Arg Ser Al
E--> 73 97 102 107
75 Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Gly Tyr Ser Thr Gly Tyr
E--> 76 112 117 122
78 Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Val Val Asn Tyr Val Leu
E--> 79 127 132 137
81 Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
E--> 82 147 152 157

Misalignment of amino acid numbering. See error summary sheet, item 3.

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```

      84 Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
E--> 85          162          167          172
      87 Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
E--> 88          177          182          187
      90 Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
E--> 91          192          197          202
      93 Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
E--> 94 207          212          217          222
      96 Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
E--> 97          227          232          237
      99 Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
E--> 100          242          247          252
      102 Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
E--> 103          257          262          267
      105 Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
E--> 106          272          277          282
      108 Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
E--> 109 287          292          297          302
      111 Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
E--> 112          307          312          317
      114 Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
E--> 115          322          327          332
      117 Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
E--> 118          337          342          347
      120 Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
E--> 121          352          357          362
185 <210> SEQ ID NO: 5
186 <211> LENGTH: 380
187 <212> TYPE: PRT
188 <213> ORGANISM: Escherichia coli
190 <220> FEATURE:
191 <221> NAME/KEY: SIGNAL
192 <222> LOCATION: (-18)..(-1)
194 <400> SEQUENCE: 5
195 Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
196 -18          -14          -9
198 Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
E--> 199          2          7          12
201 Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
E--> 202          17          22          27
204 Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
E--> 205          32          37          42
207 Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
E--> 208 47          52          57
210 Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
E--> 211          67          72          77
213 Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
E--> 214          82          87          92
216 Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln

```

RAW SEQUENCE LISTING
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```

E--> 217          97          102          107
      219 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
E--> 220          112          117          122
      222 Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
E--> 223 127          132          137          142
      225 Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
E--> 226          147          152          157
      228 Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
E--> 229          162          167          172
      231 Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
E--> 232          177          182          187
      234 Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
E--> 235          192          197          202
      237 Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
E--> 238 207          212          217          222
      240 Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
E--> 241          227          232          237
      243 Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
E--> 244          242          247          252
      246 Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
E--> 247          257          262          267
      249 Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
E--> 250          272          277          282
      252 Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
E--> 253 287          292          297          302
      255 Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
E--> 256          307          312          317
      258 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
E--> 259          322          327          332
      261 Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
E--> 262          337          342          347
      264 Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
E--> 265          352          357          362

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268 <210> SEQ ID NO: 6

269 <211> LENGTH: 1508

270 <212> TYPE: DNA

271 <213> ORGANISM: Escherichia coli

273 <400> SEQUENCE: 6

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274 ggatccgtgc actctttctt tatcgcttca ctacacattt tctcctcgca tggatgtttt      60
276 ataaaaaaca tgattgacat catgttgcat atagggttaa caaaacaagt ggcgttatct      120
278 ttttccggat tgtcttcttg tatgatatat aagttttcct cgaatgaaaa atataacttt      180
280 catttttttt attttattag catcgccatt atatgcaaat ggcgacagat tataccgtgc      240
282 tgactctaga cccccagatg aaataaaaacg ttccggaggt cttatgccca gagggcataa      300
284 tgagtacttc gatagaggaa ctcaaatagaa tattaatctt tatgatcacg cgagaggaac      360
286 acaaaccggc tttgtcagat atgatgacgg atatgtttcc acttctctta gtttgagaag      420
288 tgctcactta gcaggacagt ctatattatc aggatattcc acttactata tatatgttat      480
290 agcgacagca ccaaataatgt ttaatgttaa tgatgtatta ggcgtataca gccctcacc      540
292 atatcaggtt tctgcgttag gtggaatacc atattctcag atatatggat ggtatcgtgt      600
294 taattttggt gtgattgatg aacgattaca tcgtaacagg gaatatagag accggtatta      660

```

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Input Set : A:\PTO.PG.txt

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296	cagaaatctg	aatatagctc	cggcagagga	tggttacaga	ttagcagggtt	tcccaccgga	720
298	tcaccaagct	tggagagaag	aaccctggat	tcatcatgca	ccacaagggtt	gtggaaattc	780
300	atcaagaaca	atcacagggtg	atacttgtaa	tgaggagacc	cagaatctga	gcacaatata	840
302	tctcagggaa	tatcaatcaa	aagttaagag	gcagatattt	tcagactatc	agtcagagggt	900
304	tgacatatat	aacagaattc	gggatgaatt	atgaataaag	taaaatttta	tgttttattt	960
306	acggcggttac	tatcctctct	atgtgcacac	ggagctcctc	agtctattac	agaactatgt	1020
308	tcggaatatt	acaacacaca	aatatatacg	ataaatgaca	agatactatc	atatacggaa	1080
310	tcgatggcag	gcaaaagaga	aatgggttatc	attacattta	agagcggcgc	aacatttcag	1140
312	gtcgaagtcc	cgggcagtca	acatatagac	tcccaaaaaa	aagccattga	aaggatgaag	1200
314	gacacattaa	gaatcacata	tctgaccgag	accaaattg	ataaattatg	tgtatggaat	1260
316	aataaaaccc	ccaattcaat	tgcggaatc	agtatggaaa	actagtttgc	tttaaaagca	1320
318	tgtctaattgc	taggaaccta	tataacaact	actgtactta	tactaatgag	ccttatgctg	1380
320	catttgaaaa	ggcggtagag	gatgcaatac	cgatccttaa	actgtaacac	tataacagct	1440
322	tccactacag	ggagctgtta	tggcaaacag	aaaaaactaa	gctaggctgg	aggggcaagc	1500
324	ttggatcc						1508

E--> 325 1

E--> 329 1

delete

VERIFICATION SUMMARY

DATE: 03/28/2002

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Input Set : A:\PTO.PG.txt

Output Set: N:\CRF3\03282002\J088202.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:1508 SEQ:6
M:254 Repeated in SeqNo=6